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P#7

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/492,028

DATE: 09/27/2000

TIME: 15:37:23

Input Set : A:\Uc-926-1.app

Output Set: N:\CRF3\09272000\I492028.raw

ENTERED

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3 <110> APPLICANT: Zuker, Charles S.
4   The Regents of the University of California
6 <120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell
7   Specific G-Protein Alpha Subunit
9 <130> FILE REFERENCE: 02307E-092610US
11 <140> CURRENT APPLICATION NUMBER: US 09/492,028
12 <141> CURRENT FILING DATE: 2000-01-26
14 <150> PRIOR APPLICATION NUMBER: US 60/117,367
15 <151> PRIOR FILING DATE: 1999-01-27
17 <160> NUMBER OF SEQ ID NOS: 2
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1503
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus sp.
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (157)..(1224)
29 <223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14
30   subunit (TC-Galpha14)
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35 tcagggtggt tctcttccaa accttgctgc tgcggataat ccgcgcggcc gggcggttaag 120
37 ctccaggtcc ctgtcgctcc gtcgaggtgg caagcc atg gcc ggc tgc tgc tgt 174
38                                     Met Ala Gly Cys Cys Cys
39                                     1           5
41 ttg tct gcg gag gag aaa gag tct cag cgc atc agc gcg gag atc gag 222
42 Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu
43      10           15           20
45 cgg cac gtt cgc cgc gac aag aag gac gcg cgc cgg gag ctc aag ctg 270
46 Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu
47      25           30           35
49 ctg ttg ctg gga acc ggt gag agt ggg aaa agc acc ttt atc aag cag 318
50 Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln
51      40           45           50
53 atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc 366
54 Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly
55      55           60           65           70
57 ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg 414
58 Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met
59      75           80           85
61 atc aga gca atg gat acc ctg agg ata caa tac atg tgt gag cag aat 462
62 Ile Arg Ala Met Asp Thr Leu Arg Ile Gln Tyr Met Cys Glu Gln Asn
63      90           95           100
65 aag gaa aat gcc cag atc atc agg gaa gtg gaa gta gac aag gtc act 510
66 Lys Glu Asn Ala Gln Ile Ile Arg Glu Val Glu Val Asp Lys Val Thr
67      105           110           115

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69 gca ctc tct aga gac cag gtg gca gcc atc aag cag ctg tgg ctg gat 558
70 Ala Leu Ser Arg Asp Gln Val Ala Ala Ile Lys Gln Leu Trp Leu Asp
71 120 125 130
73 ccc gga atc cag gag tgt tac gac agg agg gag tac cag ctg tca 606
74 Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser
75 135 140 145 150
77 gac tct gcc aaa tat tac ctg acg gac att gag cgt atc gcc atg ccc 654
78 Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile Glu Arg Ile Ala Met Pro
79 155 160 165
81 tct ttc gtg cca aca caa cag gat gtg ctt cgt gtt aga gtg ccc acc 702
82 Ser Phe Val Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr
83 170 175 180
85 act ggc atc ata gaa tat cca ttc gac ctg gaa aac atc atc ttc cga 750
86 Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg
87 185 190 195
89 atg gtg gat gtt ggt ggc cag cga tct gaa cga cgg aaa tgg att cac 798
90 Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His
91 200 205 210
93 tgc ttt gag agt gtc acc tcc atc att ttc ttg gtt gct ctg agt qaa 846
94 Cys Phe Glu Ser Val Thr Ser Ile Ile Phe Leu Val Ala Leu Ser Glu
95 215 220 225 230
97 tat gac cag gtt ctg gct gag tgt gac aat gag aac cgc atg gag gag 894
98 Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn Glu Asn Arg Met Glu Glu
99 235 240 245
101 agc aaa gcc ctg ttt aga acc atc atc acc tac ccc tgg ttt ctg aac 942
102 Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Leu Asn
103 250 255 260
105 tcc tcc gtg att ctg ttc tta aac aag aag gat ctt cta gag gag aaa 990
106 Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys
107 265 270 275
109 atc atg tac tct cat cta att agc tac ttc cca gag tac aca gga cca 1038
110 Ile Met Tyr Ser His Leu Ile Ser Tyr Phe Pro Glu Tyr Thr Gly Pro
111 280 285 290
113 aag caa gat gtc aaa gcg gcc agg gac ttt atc ctg aag ctg tat caa 1086
114 Lys Gln Asp Val Lys Ala Ala Arg Asp Phe Ile Leu Lys Leu Tyr Gln
115 295 300 305 310
117 gac cag aat cct gac aaa gag aag gtt atc tat tct cac ttc act tgt 1134
118 Asp Gln Asn Pro Asp Lys Glu Lys Val Ile Tyr Ser His Phe Thr Cys
119 315 320 325
121 gct aca gac acc gag aat atc cgc ttt gtg ttt gct gct gtc aaa gac 1182
122 Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp
123 330 335 340
125 aca atc cta cag cta aac cta cgg gag ttc aac ttg gtg taa 1224
126 Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe Asn Leu Val
127 345 350 355
129 atggaggggc tactcctcgg agacagaggg tgatctgagc ccttcctgcc tgatctacaa 1284
131 gtgcttctgg accaggacct aaggacatta ttagagccac aggacagaga tgggtagtgc 1344
133 aatgtgaaaa ataccttcacc aaccttttta agtgtcttta attcttcact gtctaactct 1404
135 tttctcgcct ttggttgaa cgattaggta tcatttttga gtggttcccc ctctcctatt 1464

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137 tttttaaaact agtgttcaac agttattaaaa aaatcatgc 1503
 140 <210> SEQ ID NO: 2
 141 <211> LENGTH: 355
 142 <212> TYPE: PRT
 143 <213> ORGANISM: Mus sp.
 145 <400> SEQUENCE: 2
 146 Met Ala Gly Cys Cys Cys Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg
 147 1 5 10 15
 148 Ile Ser Ala Glu Ile Glu Arg His Val Arg Arg Asp Lys Lys Asp Ala
 149 20 25 30
 150 Arg Arg Glu Leu Lys Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys
 151 35 40 45
 152 Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser
 153 50 55 60
 154 Asp Glu Asp Arg Lys Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe
 155 65 70 75 80
 156 Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Arg Ile Gln
 157 85 90 95
 158 Tyr Met Cys Glu Gln Asn Lys Glu Asn Ala Gln Ile Ile Arg Glu Val
 159 100 105 110
 160 Glu Val Asp Lys Val Thr Ala Leu Ser Arg Asp Gln Val Ala Ala Ile
 161 115 120 125
 162 Lys Gln Leu Trp Leu Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg
 163 130 135 140
 164 Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile
 165 145 150 155 160
 166 Glu Arg Ile Ala Met Pro Ser Phe Val Pro Thr Gln Gln Asp Val Leu
 167 165 170 175
 168 Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu
 169 180 185 190
 170 Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu
 171 195 200 205
 172 Arg Arg Lys Trp Ile His Cys Phe Glu Ser Val Thr Ser Ile Ile Phe
 173 210 215 220
 174 Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn
 175 225 230 235 240
 176 Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr
 177 245 250 255
 178 Tyr Pro Trp Phe Leu Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys
 179 260 265 270
 180 Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Ile Ser Tyr Phe
 181 275 280 285
 182 Pro Glu Tyr Thr Gly Pro Lys Gln Asp Val Lys Ala Ala Arg Asp Phe
 183 290 295 300
 184 Ile Leu Lys Leu Tyr Gln Asp Gln Asn Pro Asp Lys Glu Lys Val Ile
 185 305 310 315 320
 186 Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val
 187 325 330 335
 188 Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe

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189	340	345	350.
190 Asn Leu Val			
191	355		

VERIFICATION SUMMARY

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Input Set : A:\Uc-926-1.app

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